

# SEQUENCE LISTING

<110> Han, Hui-Quan  
Kwak, Keith

<120> Human E3 Alpha Ubiquitin Ligase Family

<130> 01017/35966B

<140> To be assigned

<141> Herewith

<150> US 09/724,126

<151> 2000-11-28

<150> US 60/187,911

<151> 1999-03-08

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<170> PatentIn Ver. 2.0

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 Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile Val Gln Ala Arg Lys  
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 Ile Phe Pro Ser Val Ile Lys Tyr Val Val Glu Met Thr Ile Trp Glu  
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 His Ser Glu Asn Val Ser Gln His Pro Leu His Val Glu Val Leu His  
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Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser His	
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Tyr Cys Gln Lys His Glu Leu Asn Thr Ser Glu Ile Glu Glu Glu	
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 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu  
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 Ala Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu  
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1

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 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys  
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 Pro Tyr Cys Gln Lys His Lys Leu Ser Ser Ser Glu Val Val Glu Glu  
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 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr  
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 Asn Ile Phe Ala Ile Met Phe Arg Tyr Ala Val Asp Ile Leu Thr Trp  
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 Glu Lys Glu Ser Glu Leu Pro Glu Asp Leu Glu Val Ala Glu Lys Ser  
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 Ala Ile Gly Phe Ala Thr Thr Val Asp Arg Asp Gly Arg Arg Pro Val  
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Ser Ser Val Ala Ala His Gln Asn Phe Gly Leu Lys Ala Leu Ser Trp  
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 Val Tyr His Gln Leu Phe Met Ser Ser Leu Leu Met Asp Leu Lys Tyr  
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 Cys Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln  
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Ala Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr  
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Ser Cys Gly Ser Gly Ala Gly Ile Phe Leu Arg Val Arg Glu Cys Gln  
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Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro  
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Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn  
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Pro Leu His Leu Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp  
1715 1720 1725

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23

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Val	Asp	Phe	Tyr	Thr	Ala	Phe	Leu	His	His	Leu	Ala	Gln	Leu	Val	Pro	35	40	45	
Glu	Ile	Tyr	Phe	Ala	Glu	Met	Asp	Pro	Asp	Leu	Glu	Lys	Gln	Glu	Glu	50	55	60	
Ser	Val	Gln	Met	Ser	Ile	Leu	Thr	Pro	Leu	Glu	Trp	Tyr	Leu	Phe	Gly	65	70	75	80
Glu	Asp	Pro	Asp	Ile	Cys	Leu	Glu	Lys	Leu	Lys	His	Ser	Gly	Ala	Phe	85	90	95	
Gln	Leu	Cys	Gly	Lys	Val	Phe	Lys	Ser	Gly	Glu	Thr	Thr	Tyr	Ser	Cys	100	105	110	
Arg	Asp	Cys	Ala	Ile	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe	115	120	125	
Gln	Ser	Ser	Val	His	Lys	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr	130	135	140	
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly	145	150	155	160
Pro	Phe	Cys	Val	Asp	His	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Thr	Lys	Glu	165	170	175	
Ser	Leu	His	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	Ala	Gln	Ala	Arg	Arg	180	185	190	
Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Ile	Val	Glu	Met	Thr	Ile	Trp	Glu	195	200	205	
Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	210	215	220	
Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	225	230	235	240
Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	245	250	255	
Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	260	265	270	
Ala	Gly	Val	Tyr	Ala	Thr	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	275	280	285	
His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	290	295	300	
Ser	Val	Val	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	305	310	315	320
Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	325	330	335	

Gln	Ala	Cys	Leu	Val	Glu	Glu	Pro	Gly	Ser	Glu	Asn	Pro	Cys	Leu	Ile	340	345	350
Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	355	360	365
Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	370	375	380
Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	385	390	400
Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Glu	Arg	Ser	Ile	Ser	Ile	Thr	Ala	405	410	415
Leu	Ser	Val	Gln	Met	Leu	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	420	425	430
Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	435	440	445
Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	Asn	Phe	Gln	Gly	Tyr	450	455	460
Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	Ile	Cys	Asp	Leu	Lys	465	470	475
Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Val	Ile	Trp	Thr	Glu	Arg	Leu	Arg	Ala	485	490	495
Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys	Ile	Leu	Thr	Cys	Met	500	505	510
Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Val	515	520	525
Asp	Pro	Asp	Trp	Glu	Ala	Ala	Ile	Ala	Ile	Gln	Met	Gln	Leu	Lys	Asn	530	535	540
Ile	Leu	Leu	Met	Phe	Gln	Glu	Trp	Cys	Ala	Cys	Asp	Glu	Asp	Leu	Leu	545	550	555
Leu	Val	Ala	Tyr	Lys	Glu	Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr	565	570	575
Asn	Phe	Met	Ser	Ser	Thr	Lys	Thr	Val	Val	Gln	Leu	Cys	Gly	His	Ser	580	585	590
Leu	Glu	Thr	Lys	Ser	Tyr	Lys	Val	Ser	Glu	Asp	Leu	Val	Ser	Ile	His	595	600	605
Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His	Val	Arg	Leu	Ser	Arg	610	615	620
Leu	Gly	Ala	Ile	Ser	Arg	Leu	His	Glu	Phe	Val	Pro	Phe	Asp	Ser	Phe	625	630	635
Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg	Cys	Leu	Val	Leu	Val	645	650	655
Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn	Gly	Leu	Ser	Leu	Ile	660	665	670

Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys	Arg	Glu	Glu	Met	Tyr		
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Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	Ser	Ile	Met	Asp	Pro		
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Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile	Val	Gly		
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Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	Arg	Glu	Glu	Val	Ile		
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Met	Arg	Glu	Ile	Thr	His	Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro	His	Ser		
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Met	Tyr	Phe	Tyr	His	Tyr	Ser	Lys	Thr	Gln	His	Ser	Lys	Ala	Glu	His		
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Met	Gln	Lys	Lys	Arg	Arg	Lys	Gln	Glu	Asn	Lys	Asp	Glu	Ala	Leu	Pro		
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Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	Ser	Lys	Val	Val	Asn		
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Arg	Ala	Val	Asp	Thr	Glu	Ser	Asn	Leu	Trp	Thr	Glu	Gly	Met	Leu	Gln		
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Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	Glu	Glu	Lys	Gln	Gln		
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Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Val	Ala	Phe	Asp	Phe	Tyr	His	Lys		
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			980					985					990				
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 Arg Gly Pro Ala Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys  
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 Val Asp His Leu Gly Glu Thr Leu Asp Pro Leu Phe Met Asp Pro Asp  
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 Leu Ala His Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met His Ala  
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 Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser Gln Gln  
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 Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu Gly  
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Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Ser Gly Leu Lys  
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 Thr Val Asp Leu Gln Pro Ser Pro Leu Ser Ser Ser Tyr Asn His Leu  
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 Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu  
 1445 1450 1455  
 Thr Thr Asp Thr Asp Leu Ser Pro Gly Pro Pro Leu Ala Glu Gly Glu  
 1460 1465 1470  
 Glu Asp Ser Glu Glu Ala Arg Cys Ala Ser Ala Phe Phe Val Glu Val  
 1475 1480 1485  
 Ser Gln His Thr Asp Gly Leu Thr Gly Cys Gly Ala Pro Gly Trp Tyr  
 1490 1495 1500  
 Leu Trp Leu Ser Leu Arg Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala  
 1505 1510 1515 1520  
 Ala Leu Leu Phe His Tyr Leu Leu Gly Val Ala Pro Pro Glu Glu Leu  
 1525 1530 1535  
 Phe Ala Asn Ser Ala Glu Gly Glu Phe Ser Ala Leu Cys Ser Tyr Leu  
 1540 1545 1550  
 Ser Leu Pro Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr  
 1555 1560 1565  
 Ile Arg Pro Leu Leu Gln Arg Trp Cys Gly Asp Pro Ala Leu Leu Lys  
 1570 1575 1580  
 Ser Leu Lys Gln Lys Ser Ala Val Val Arg Tyr Pro Arg Lys Arg Asn  
 1585 1590 1595 1600  
 Ser Leu Ile Glu Leu Pro Glu Asp Tyr Ser Cys Leu Leu Asn Gln Ala  
 1605 1610 1615  
 Ser His Phe Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro  
 1620 1625 1630  
 Val Leu Cys Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys  
 1635 1640 1645  
 Cys Gln Glu Ile Val Asn Gly Glu Glu Val Gly Ala Cys Val Phe His  
 1650 1655 1660  
 Ala Leu His Cys Gly Ala Gly Val Cys Ile Phe Leu Lys Ile Arg Glu  
 1665 1670 1675 1680

Cys Arg Val Val Leu Val Glu Gly Lys Ala Arg Gly Cys Ala Tyr Pro  
1685 1690 1695

Ala Pro Tyr Leu Asp Glu Tyr Gly Glu Thr Asp Pro Gly Leu Lys Arg  
1700 1705 1710

Gly Asn Pro Leu His Leu Ser Arg Glu Arg Tyr Arg Lys Leu His Leu  
1715 1720 1725

Val Trp Gln Gln His Cys Ile Ile Glu Glu Ile Ala Arg Ser Gln Glu  
1730 1735 1740

Thr Asn Gln Met Leu Phe Gly Phe Asn Trp Gln Leu Leu  
1745 1750 1755

<210> 16  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 16  
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

<210> 17  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 17  
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1 5 10 15

<210> 18  
<211> 5205  
<212> DNA  
<213> Homo sapiens

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catcatttg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttggaa 180  
aagcaggagg aaagtgtaca aatgtcaata ttcactccac tggaatggta cttattttgga 240  
gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300  
agggttttca aaagtggaga gacaacctat tcttgcaggg attgtgcaat tgatccaaca 360  
tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420  
catacttcta ctggaggagg gttctgtgac tgtggagaca cagaggcatg gaaaactggc 480

cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540  
ccgttgaatg aagaggtaat tgtccaagcc aggaaaatat ttccttcagt gataaaatat 600  
gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctctgaact ccagataagg 660  
knryycvndh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720  
gccagttgc ataccactgc cattgacaaa gagggtcgtc gggctgttaa agcgggagct 780  
tatgctgctt gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa 840  
catccacttc atgtagaagt attacactca gagattatgg ctcatcagaa atttgctttg 900  
cgtcttggtt cctggatgaa caaaattatg agctattcaa gtgactttag gcagatcttt 960  
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agcagttttt ttatggagat ggaatacaaaa aaactctttg ctatggaatt tgtgaagtat 1140  
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gaagaaatcc gaagacagg tgggcaacac attgaagtgg atcctgattg ggaggctgcc 1560  
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gatgaagaac tcttacttgt ggcttataaa gaatgtcaca aagctgtgat gaggtgcagt 1680  
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gttgccagg ttgttgctga gatgtggcga agaaatggac tgtctcttat tagccagggtg 1980  
ttttattacc aagatgttaa gtgcagagaa gaaatgtatg ataaagatat catcatgctt 2040  
cagattggtg catctttaat ggatcccaat aagttcttgt tactgggtact tcagaggtat 2100  
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gtacctggag tgggaaatgt gaccaaagaa gaggtcacia tgagagaaat cattcacttg 2280  
ctttgcattg aacccatgcc acacagtgcc attgccaaa atttacctga gaatgaaaat 2340  
aatgaaactg gcttagagaa tgtcataaac aaagtggcca catttaagaa accagggtgta 2400



tcaggccatg gagtttatga actaaaagat gaatcactga aagacttcaa tatgtacttt 2460  
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 caagaaaaca aagatgaagc attgccgcca ccaccacctc ctgaattctg ccctgctttc 2580  
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 caaaagataa acagtgagaa tgcagatgct cthgtcaac thtgacctc ggcacgggtg 3660  
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 ctgagthttg gcgttgagtc thcgattaaa tattcaaata gcatcaagga aatggthatt 3840  
 ctctthgcca caacaattta tagaattgga thgaaagtgc cacctgatga aagggatcct 3900  
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 cggaagctcc atttggtctg gcaacaacac tgcattatag aagagattgc taggagccaa 5160  
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<210> 19  
 <211> 1735  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
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 20 25 30  
 Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala Phe Leu His His Leu  
 35 40 45  
 Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu  
 50 55 60  
 Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu  
 65 70 75 80  
 Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys  
 85 90 95  
 His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu  
 100 105 110  
 Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu  
 115 120 125  
 Cys Met Asp Cys Phe Gln Asp Ser Val His Lys Asn His Arg Tyr Lys  
 130 135 140

Met	His	Thr	Ser	Thr	Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	145	150	155	160
Ala	Trp	Lys	Thr	Gly	Pro	Phe	Cys	Val	Asn	His	Glu	Pro	Gly	Arg	Ala	165	170	175	
Gly	Thr	Ile	Lys	Glu	Asn	Ser	Arg	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	180	185	190	
Val	Gln	Ala	Arg	Lys	Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Val	Val	Glu	195	200	205	
Met	Thr	Ile	Trp	Glu	Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	210	215	220	
Arg	Glu	Lys	Asn	Glu	Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	225	230	235	240
His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	245	250	255	
Glu	Leu	Ala	Glu	Ala	Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	260	265	270	
Arg	Arg	Ala	Val	Lys	Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys	275	280	285	
Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	290	295	300	
Val	Glu	Val	Leu	His	Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	305	310	315	320
Arg	Leu	Gly	Ser	Trp	Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	325	330	335	
Arg	Gln	Ile	Phe	Cys	Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu	340	345	350	
Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	355	360	365	
Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	370	375	380	
Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	385	390	395	400
Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser	405	410	415	
Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu	420	425	430	
Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	435	440	445	
Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	450	455	460	
Asn	Phe	Gln	Gly	Tyr	Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	465	470	475	480

Ile Cys Asp Leu Lys Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr  
 485 490 495  
 Glu Arg Leu Arg Met Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys  
 500 505 510  
 Ile Leu Thr Cys Met Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly  
 515 520 525  
 Gln His Ile Glu Val Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln  
 530 535 540  
 Met Gln Leu Lys Asn Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys  
 545 550 555 560  
 Asp Glu Glu Leu Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val  
 565 570 575  
 Met Arg Cys Ser Thr Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln  
 580 585 590  
 Ser Cys Gly His Ser Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp  
 595 600 605  
 Leu Val Ser Ile His Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His  
 610 615 620  
 Val Arg Leu Ser Arg Leu Gly Ala Val Ser Arg Leu His Glu Phe Val  
 625 630 635 640  
 Ser Phe Glu Asp Phe Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg  
 645 650 655  
 Cys Leu Val Leu Val Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn  
 660 665 670  
 Gly Leu Ser Leu Ile Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys  
 675 680 685  
 Arg Glu Glu Met Tyr Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala  
 690 695 700  
 Ser Leu Met Asp Pro Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr  
 705 710 715 720  
 Glu Leu Ala Glu Ala Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp  
 725 730 735  
 Leu Ile Lys Gln Tyr Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu  
 740 745 750  
 Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr  
 755 760 765  
 Lys Glu Glu Val Thr Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu  
 770 775 780  
 Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn  
 785 790 795 800  
 Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys  
 805 810 815

Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser  
 820 825 830  
 Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His  
 835 840 845  
 Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys  
 850 855 860  
 Asp Glu Ala Leu Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe  
 865 870 875 880  
 Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu  
 885 890 895  
 Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr  
 900 905 910  
 Glu Gly Met Leu Gln Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu  
 915 920 925  
 Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe  
 930 935 940  
 Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile  
 945 950 955 960  
 Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln  
 965 970 975  
 Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg  
 980 985 990  
 Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu  
 995 1000 1005  
 Ser Ile Lys Asn Asp Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg  
 1010 1015 1020  
 Lys Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala  
 1025 1030 1035 1040  
 Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met  
 1045 1050 1055  
 Tyr Asp Asn Thr Ser Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu  
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 Glu Glu Ser Thr Pro Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly  
 1075 1080 1085  
 Pro Lys Arg Gly Pro Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile  
 1090 1095 1100  
 Leu Cys Gln Glu Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val  
 1105 1110 1115 1120  
 Leu Ser Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly  
 1125 1130 1135  
 Lys Pro Ile Glu Leu Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp  
 1140 1145 1150

Pro Asp Leu Ala Tyr Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met  
 1155 1160 1165  
 His Ala Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser  
 1170 1175 1180  
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 Pro Leu Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala  
 1220 1225 1230  
 Gln Leu Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile  
 1235 1240 1245  
 Ser Gly Tyr Asn Ile Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile  
 1250 1255 1260  
 Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile  
 1265 1270 1275 1280  
 Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys  
 1285 1290 1295  
 Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys  
 1300 1305 1310  
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 1315 1320 1325  
 Thr Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu  
 1330 1335 1340  
 Gly Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu  
 1345 1350 1355 1360  
 Lys Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln  
 1365 1370 1375  
 Val Leu Ile Gln Lys His Leu Val Arg Leu Leu Ser Val Val Leu Pro  
 1380 1385 1390  
 Asn Ile Lys Ser Glu Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe  
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 1425 1430 1435 1440  
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 1445 1450 1455  
 Leu Thr Val Asp Thr Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser  
 1460 1465 1470  
 Glu Glu Ala His Ser Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr  
 1475 1480 1485

Thr Ser Gly Ser Ile Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val  
 1490 1495 1500  
 Ser Leu Lys Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe  
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 Phe His Tyr Leu Leu Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn  
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 Ser Ala Glu Gly Glu Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro  
 1540 1545 1550  
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 1570 1575 1580  
 Gln Lys Asn Thr Val Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile  
 1585 1590 1595 1600  
 Glu Leu Pro Asp Asp Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe  
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 Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys  
 1620 1625 1630  
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 Ile Val Asn Gly Glu Glu Val Gly Ala Cys Ile Phe His Ala Leu His  
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 Cys Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr  
 1665 1670 1675 1680  
 Gly Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser  
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 Arg Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer

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22

<210> 21  
 <211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
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 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 22  
 aggaagctgt ggatcatgt 18  
  
 <210> 23  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
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